

WEST Search History

DATE: Tuesday, November 18, 2003

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
L4	L3 same consensus	3	L4
L3	(taci or bcma) same april	33	L3
L2	Theill-Lars-\$.in.	7	L2
<i>DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
L1	Theill-Lars-\$.in.	3	L1

END OF SEARCH HISTORY

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 06:14:12 ; Search time 68 seconds
(without alignments)
307.386 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEFDLLHACIPQCLR.....SEYFDSLHACPPATCPQC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	20.2	1792	13 O57484	O57484 gallus gall
2	94.5	19.0	223	11 Q62220	Q62220 mus musculus
3	94.5	19.0	230	11 Q64507	Q64507 mus musculus
4	93.5	18.8	195	11 Q9D141	Q9D141 mus musculus
5	93.5	18.8	774	5 Q8IT70	Q8IT70 hydra atten
6	93	18.7	353	4 Q8NBS9	Q8NBS9 homo sapien
7	92.5	18.6	169	4 Q4J564	Q4J564 homo sapien
8	92	18.5	217	11 Q8BV88	Q8BV88 mus musculus
9	91.5	18.4	136	4 Q9BYR5	Q9BYR5 homo sapien
10	91.5	18.4	186	4 Q9BYR2	Q9BYR2 homo sapien
11	91.5	18.4	186	11 Q64526	Q64526 mus musculus
12	91.5	18.4	191	11 Q9D3H7	Q9D3H7 mus musculus
13	89	17.9	159	4 Q9BYQ3	Q9BYQ3 homo sapien
14	89	17.9	1574	11 Q88281	Q88281 rattus norv
15	88	17.7	166	4 Q9BYR3	Q9BYR3 homo sapien
16	87.5	17.6	154	4 Q9BYQ2	Q9BYQ2 homo sapien

17	87.5	17.6	174	4 Q9BYQ4	Q9BYQ4 homo sapien
18	87.5	17.6	193	4 Q9BYQ5	Q9BYQ5 homo sapien
19	87	17.5	159	4 Q9BYQ0	Q9BYQ0 homo sapien
20	87	17.5	165	11 Q9D7P3	Q9D7P3 mus musculus
21	87	17.5	1376	5 Q8SZS2	Q8SZS2 drosophila
22	86	17.3	101	11 Q8BR19	Q8BR19 mus musculus
23	86	17.3	188	11 Q70148	Q70148 rattus norv
24	86	17.3	2112	5 Q8WPL0	Q8WPL0 oikopleura
25	85.5	17.2	154	4 Q9BYP9	Q9BYP9 homo sapien
26	85.5	17.2	177	11 Q9D644	Q9D644 mus musculus
27	85.5	17.2	189	11 Q9D5Z7	Q9D5Z7 mus musculus
28	85	17.1	177	11 Q8CAY5	Q8CAY5 mus musculus
29	85	17.1	202	11 Q91W93	Q91W93 mus musculus
30	85	17.1	221	13 Q8AXC1	Q8AXC1 xenopus lae
31	85	17.1	286	13 Q8AXC0	Q8AXC0 xenopus lae
32	85	17.0	325	10 Q94HS1	Q94HS1 oryza sativ
33	84.5	17.0	767	13 Q9DGR2	Q9DGR2 xenopus lae
34	84	16.9	195	4 Q9BYQ6	Q9BYQ6 homo sapien
35	84	16.9	201	4 Q9BQ66	Q9BQ66 homo sapien
36	84	16.9	210	4 Q9BYR0	Q9BYR0 homo sapien
37	84	16.9	466	11 Q8BTN5	Q8BTN5 mus musculus
38	84	16.9	947	11 Q8BKK7	Q8BKK7 mus musculus
39	84	16.9	1671	5 Q9NJV5	Q9NJV5 biomphalari
40	83.5	16.8	110	5 Q9BIR2	Q9BIR2 paramecium
41	83.5	16.8	130	11 Q9Z287	Q9Z287 mus musculus
42	83.5	16.8	191	4 Q9BYQ8	Q9BYQ8 homo sapien
43	83	16.7	175	4 Q07628	Q07628 homo sapien
44	82.5	16.6	1145	11 Q8BMN9	Q8BMN9 mus musculus
45	82.5	16.6	1450	11 Q8JZW7	Q8JZW7 mus musculus

ALIGNMENTS

RESULT 1

O57484 ID O57484 PRELIMINARY; PRT; 1792 AA.

AC O57484;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Laminin beta 2-like chain.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93015947; PubMed=1400373;

RA O'Rear J.J.;

RT "A novel laminin B1 chain variant in avian eye.";

RL J. Biol. Chem. 267:20555-20557(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98209634; PubMed=9550264;

RA Liu J., Swadison S., Xie W., Brewton R.G., Mayne R.;

RT "Primary structure and expression of a chicken laminin beta chain:

RL evidence for four beta chains in birds.";

RL Matrix Biol. 16:471-481(1998).

DR EMBL; AF038555; AAB92586.1; -.

DR HSP; P02468; 1KLO

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR001886; LamNT.

DR Pfam; PF00053; laminin_EGF; 13.

DR Pfam; PF00055; laminin_Nterm; 1.

DR PRINTS; PR00011; EGFLAMININ.

DR SMART; SM00180; EGF Lam; 13.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF_1; 10.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.

KW Laminin EGF-like domain.
SQ SEQUENCE 1792 AA; 195723 MW; 4A4CBE0206F6A600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
Best Local Similarity 32.0%; Pred. No. 0.0013;
Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDSLHACIPQCLRCSSN---TPPLTC---QRYCCYFDSLHACP-----CLR 49
Db 1017 COPGYGDAMRISC-----RRCNVLGTDPNTGCGQCCQDORSQCHCLPHVEGQSCDR 1072
QY 50 CSP-----PTQYCCFHSYFDSLHACPPATCQPYC 81
Db 1073 CSPNFWNLGSGGQCEPCACHPQH---SLSPACNQFTQCSC 1110

RESULT 2
Q62220
AC Q62220 PRELIMINARY; PRT; 223 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine 2 ultra high sulfur protein.
GN KRTAP5-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=91065960; PubMed=2250030;
RA Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Serine-rich ultra high sulfur protein gene expression in murine hair
and skin during the hair cycle."
RL J. Biol. Chem. 265:21375-21380(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=91065960; PubMed=2250030;
RA Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Serine-rich ultra high sulfur protein gene expression in murine hair
and skin during the hair cycle."
RL J. Biol. Chem. 265:21375-21380(1990).
RN [2]

QY 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCLRCSPPTQYCCF 60
Db 149 CCQSS-----CCKPC---CSSGCGSSCCQSSCK-----PCC-CQSSCKPCCC 188
QY 61 HSEYFDSLHACPPATCQPYC 81
Db 189 QSS-----CCKPCCCQSSC 202

Query Match 19.0%; Score 94.5; DB 11; Length 230;
Best Local Similarity 29.6%; Pred. No. 0.0012;
Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCLRCSPPTQYCCF 60
Db 149 CCQSS-----CCKPC---CSSGCGSSCCQSSCK-----PCC-CQSSCKPCCC 188
QY 61 HSEYFDSLHACPPATCQPYC 81
Db 189 QSS-----CCKPCCCQSSC 202

RESULT 4
Q9D141
ID Q9D141 PRELIMINARY; PRT; 195 AA.
AC Q9D141
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 18 days embryo cDNA, RIKEN full-length enriched library,
clone:1110030N11, full insert sequence.
DE clone:1110030N11, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Wagner L., Washio T.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR ENBL: AK003994; BAB23112.1; --
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001010; Thionin.

KW Laminin EGF-like domain.
SQ SEQUENCE 1792 AA; 195723 MW; 4A4CBE0206F6A600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
Best Local Similarity 32.0%; Pred. No. 0.0013;
Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDSLHACIPQCLRCSSN---TPPLTC---QRYCCYFDSLHACP-----CLR 49
Db 1017 COPGYGDAMRISC-----RRCNVLGTDPNTGCGQCCQDORSQCHCLPHVEGQSCDR 1072
QY 50 CSP-----PTQYCCFHSYFDSLHACPPATCQPYC 81
Db 1073 CSPNFWNLGSGGQCEPCACHPQH---SLSPACNQFTQCSC 1110

RESULT 2
Q62220
AC Q62220 PRELIMINARY; PRT; 223 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine 2 ultra high sulfur protein.
GN KRTAP5-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=91065960; PubMed=2250030;
RA Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Serine-rich ultra high sulfur protein gene expression in murine hair
and skin during the hair cycle."
RL J. Biol. Chem. 265:21375-21380(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=91065960; PubMed=2250030;
RA Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Serine-rich ultra high sulfur protein gene expression in murine hair
and skin during the hair cycle."
RL J. Biol. Chem. 265:21375-21380(1990).
RN [2]

QY 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCLRCSPPTQYCCF 60
Db 150 CCQSS-----CCKPC---CSSGCGSSCCQSSCK-----PCC-CQSSCKPCCC 189
QY 61 HSEYFDSLHACPPATCQPYC 81
Db 190 QSS-----CCKPCCCQSSC 203

Query Match 19.0%; Score 94.5; DB 11; Length 223;
Best Local Similarity 29.6%; Pred. No. 0.0011;
Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCLRCSPPTQYCCF 60
Db 150 CCQSS-----CCKPC---CSSGCGSSCCQSSCK-----PCC-CQSSCKPCCC 189
QY 61 HSEYFDSLHACPPATCQPYC 81
Db 190 QSS-----CCKPCCCQSSC 203

RESULT 3
Q64507
ID Q64507 PRELIMINARY; PRT; 230 AA.
AC Q64507
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine 1 ultra high sulfur protein.
GN KRTAP5-1.
OS Mus musculus (Mouse).

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RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yanashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuna M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.
DR ENBL; AK090647; BAC03496.1; -.
DR InterPro; IPR003006; IG_MHC.
DR PROSITE; PS00290; IG_MHC; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 353 AA; 38653 MW; 61EC03AA375681E2 CRC64;

Query Match 18.7%; Score 93; DB 4; Length 353;
Best Local Similarity 32.9%; Pred. No. 0.0025;
Matches 27; Conservative 2; Mismatches 19; Indels 34; Gaps 65

QY 11 LHACIPCOLRCSNNPPLTTCORYCEYFDSLHACPC--LR CSP---PTCQVCCFHSEYF 65
DB 76 LHCSFCCSLR CSP-----CCS-----LHCSPPCSLR CSPCCSLR CSPCC----- 114

QY 66 DSLHACFPAT-----CQPYC 81
DB 115 --SLHCSPPCSLQCSLHCSPHC 134

RESULT 7
Q14564 PRELIMINARY; PRT; 169 AA.
ID Q14564;
AC Q14564;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE High-sulphur keratin.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Drabant B., Doenecke D.;
RA "Nucleotide sequence of a Human high-sulphur keratin cDNA.";
RL Submitted (DEC-1991) to the ENBL/GenBank/DBJ databases.
DR ENBL; X63755; CAA45283.1; -.
DR HSP; P01064; IPT2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001138; Fungi_TnR.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR 1; 1.
DR PROSITE; PS00463; ZN2_CY6_FUNGAL 1; 1.
SQ SEQUENCE 169 AA; 16216 MW; A39206EB0B49D4BE CRC64;

Query Match 18.6%; Score 92.5; DB 4; Length 169;
Best Local Similarity 30.0%; Pred. No. 0.0015;
Matches 27; Conservative 5; Mismatches 37; Indels 21; Gaps 51

QY 1 CSQNEYFDSLHACIPCOLRCSNNPPLTTCORYCEYFDSLHAC-PCLR-----CS 51
DB 77 CSQ-----CSCCKPC--CCSSCGSSCCCKPYCSCCKPCSSSGRGSSCCQ 127

QY 52 PFTCQVCCFHSEYFDSLHACFPATCOPYC 81
DB 128 SSCCKPCSSSGCGSS---CCQSSCKCPCC 154

RESULT 8
Q8BV88

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DR PROSITE; PS01208; VWFC; 1.
SQ SEQUENCE 186 AA; 19658 MW; 61D6BFDAB72CFEB4 CRC64;

Query Match      18.4%; Score 91.5; DB 11; Length 186;
Best Local Similarity 34.7%; Pred. No. 0.0022;
Matches 25; Conservative 4; Mismatches 24; Indels 19; Gaps 6;

QY 14 CIP-CQLRC--SSNTPLTCQRYCCYFDSLHAC--PCLRCSPPTQYCCFHSEYFDSL 69
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 85 CQPCQPCQSCQSCQPCRCISCCQPC--CRPSCQSCS----- 132
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 70 HACPPATCQPYC 81
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 133 --CRPC-CQFFC 141
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 12
Q9D3H7 PRELIMINARY; PRT; 191 AA.
ID Q9D3H7
AC Q9D3H7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 10 days neonate head cDNA, RIKEN full-length enriched library,
DE clone:530401l02, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo T., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017437; BAB30743.1; --
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001010; Thionin.
DR InterPro: IPR001368; TNFR_c6.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF01500; Keratin_B2; 1.
DR PROSITE: PS00271; THIONIN; 1.
DR PROSITE: PS00852; TNFR_NGFR_1; 1.
DR PROSITE: PS01208; VWFC; 1.
SQ SEQUENCE 191 AA; 20088 MW; 522B841DC9A8A9D5 CRC64;

Query Match      18.4%; Score 91.5; DB 11; Length 191;
Best Local Similarity 32.9%; Pred. No. 0.0023;
Matches 23; Conservative 3; Mismatches 21; Indels 23; Gaps 5;

QY 16 PCQLRCSSNTP--PLTCQRYCCYFDSLHACPLRCSPPTCQ--YCCFHSEYFDSLHA 71
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 63 PCVSSCRTPCQPCCVSSCCQ-----PC--CQPCQSCQSCQPS-----C 103
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 72 CPPATCQPYC 81
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Db 104 CQSCCQPC 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
Q9BYQ3 PRELIMINARY; PRT; 159 AA.
ID Q9BYQ3
AC Q9BYQ3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Keratin associated protein 9.3.
GN KRTAP9.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Scalp;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
RT "Characterization of a cluster of human high/ultrahigh keratin
RT associated proteins on chromosome 17q12-21.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ406947; CAC27586.1; --
DR Genew: HGNC:16927; KRTAP9-3.
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF01500; Keratin_B2; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
SQ SEQUENCE 159 AA; 16853 MW; 375CC1B52BECDE68 CRC64;

Query Match      17.9%; Score 89; DB 4; Length 159;
Best Local Similarity 29.5%; Pred. No. 0.0038;
Matches 26; Conservative 4; Mismatches 20; Indels 38; Gaps 7;

QY 10 LHHACIP-CQLRC-----SSNTPLTCQRYCCYFDSLHAC--PCLRCSP 53
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 MTHCCSPCCQTCCTTCQWQTTTCSTP--CCQSCC-----VSSCCQPC--CHPT 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 54 TCQYCCFHSEYFDSLHACPPATCQPYC 81
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 51 CQNTC-----CRTTCQPC 66
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
Q88281 PRELIMINARY; PRT; 1574 AA.
ID Q88281
AC Q88281
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MEGF6.
GN MEGF6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98360089; PubMed=98303030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL: AB011532; BAA32462.1; --
DR HSP: P00736; IAPQ.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR Pfam: PF00008; EGF; 24.
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Search completed: November 12, 2003, 06:28:21
Job time : 70 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 06:14:12 ; Search time 70 Seconds
(without alignments)
183.669 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEFDSLHACIPQLR.....SEYFDSLHACPPATQPYC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205	41.2	302	22	Human BCMA-Immunog
2	205	41.2	302	22	Mouse IgG signal/h
3	201.5	40.5	283	23	Human BCMA-Immunog
4	201	40.4	34	23	Human B-cell matur
5	201	40.4	51	23	Human B-cell matur
6	201	40.4	58	23	Human B-cell matur
7	201	40.4	181	23	Human B-cell matur
8	201	40.4	184	21	Amino acid sequenc
9	201	40.4	184	21	A human BCMA prote

10	201	40.4	184	22	AAE09241	Human BCMA protein
11	201	40.4	184	22	AAE00506	Human B cell matur
12	201	40.4	184	22	AAE00898	Human BAFF recepto
13	201	40.4	184	22	AAE00898	Human B cell matur
14	201	40.4	184	23	AAE00898	Human B-cell matur
15	201	40.4	184	23	AAE00898	Metastatic colorec
16	201	40.4	184	23	AAE00898	Human BCMA recepto
17	201	40.4	184	24	AAE00898	Human B-cell matur
18	201	40.4	184	24	AAE00898	Amino acid sequenc
19	201	40.4	184	24	AAE00898	Human tumour necro
20	201	40.4	184	24	AAE00898	Human translocatio
21	159.5	32.0	288	23	AAE00898	Human BAFF recepto
22	153	30.7	24	23	AAE00898	Human-murine BCMA
23	153	30.7	117	23	AAE00898	Human-murine B cel
24	139.5	28.0	281	23	AAE00898	Mouse BCMA-human 1
25	136	27.3	185	21	AAE00898	Amino acid sequenc
26	136	27.3	185	22	AAE00898	Murine B cell matur
27	124	24.9	42	24	AAE00898	TALI-1 related pro
28	124	24.9	42	24	AAE00898	Human TACI (dl-29,
29	114	22.9	344	24	AAE00898	Human TACI (dl-29,
30	106	21.3	332	24	AAE00898	Human TACI-FC5 fus
31	106	21.3	348	24	AAE00898	Human TACI (dl-29,
32	100.5	20.2	334	23	AAE00898	Protein of hTACI (
33	100.5	20.2	366	23	AAE00898	Protein of hTACI (
34	99.5	20.0	357	24	AAE00898	Human TACI (dl-29,
35	98	19.7	249	21	AAE00898	A murine tnfr4, a
36	96.5	19.4	301	22	AAE00898	Human protein SEQ
37	95	19.1	256	22	AAE00898	Novel human diagno
38	95	19.1	351	22	AAE00898	Human lymphocyte s
39	93	18.7	166	19	AAE00898	Human TACI extrac
40	93	18.7	166	23	AAE00898	Human TACI splice
41	93	18.7	265	22	AAE00898	Human TACI splice
42	93	18.7	265	22	AAE00898	Amino acid sequenc
43	93	18.7	291	23	AAE00898	Human AGP-3 recept
44	93	18.7	293	19	AAE00898	Human lymphocyte s
45	93	18.7	293	21	AAE00898	Human neutrokinine-a

ALIGNMENTS

RESULT 1

AAE00507

ID AAE00507 standard; Protein; 302 AA.

XX AAE00507;

AC AAE00507;

XX 31-JUL-2001 (first entry)

XX Human BCMA-Immunoglobulin G Fc region fusion construct.

DE Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;

XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;

XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;

XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;

XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;

XX organ transplantation; HIV; human immunodeficiency virus; TNF; murine;

XX tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;

XX immunoglobulin G; IgG; Fc region.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX Key Location/Qualifiers

FT 1..22 /label= Signal peptide

FT /note= "Derived from murine Ig kappa sequence"

FT 23..302 /label= Mature_human_BCMA_IgG_Fc_fusion_protein

FT 23..75 /note= "Derived from human BCMA protein"

FT 76..302 /note= "Derived from human IgG Fc region"

FT 76..302 /note= "Derived from human IgG Fc region"


```

FT Domain 24..302
FT /label= Cysteine rich domain
FT /note= "Derived from human BCMA"
XX
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX
XX 11-FEB-2000; 2000US-0181807.
XX
XX 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX (APOT-) APOTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
XX WPI; 2001-266242/27.
XX
XX N-PSDB; AAD03847.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor
XX (APRIL-R) antagonist -
XX
XX Example 1; Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or
XX carcinoma. The method involves administering a composition comprising
XX A proliferation inducing ligand receptor (APRIL-R) also referred as
XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and
XX human immunodeficiency virus (HIV), and for treating, suppressing or
XX altering an immune response involving a signalling pathway between
XX APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX The present sequence is a fusion construct containing human APRIL-R
XX also referred as BCMA or BCM protein, Fc region of human immunoglobulin
XX G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX Sequence 302 AA;
XX
XX Query Match 41.2%; Score 205; DB 22; Length 302;
XX Best Local Similarity 67.8%; Pred. No. 3.1e-10;
XX Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX 1 CSQNEYFDSLHACIPCOLRCSNTPTLTQRYC-CYFDSL-----LHACPCLRCSP 53
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 31 CSQNEYFDSLHACIPCOLRCSNTPTLTQRYC-CYFDSL-----LHACPCLRCSP 87
XX
XX RESULT 2
XX AAB60699
XX ID AAB60699 standard; Protein; 302 AA.
XX
XX AC AAB60699;
XX
XX DT 22-MAY-2001 (first entry)
XX
XX DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
XX
XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;

```

```

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX
XX Chimeric - Homo sapiens.
XX
XX Chimeric - Mus sp.
XX
XX WO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000WO-US22507.
XX
XX 17-AUG-1999; 99US-0149378.
XX
XX 11-FEB-2000; 2000US-0181684.
XX
XX 18-FEB-2000; 2000US-0183536.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX (APOT-) APOTECH R & D SA.
XX
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX
XX WPI; 2001-202866/20.
XX
XX N-PSDB; AAF5999.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
XX antibody homolog -
XX
XX Example 4; Fig 2; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders. B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAFF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAFF-R
XX proteins or BAFF-R specific antibodies may be used for treating,
XX suppressing or altering an immune response involving a signalling pathway
XX between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
XX comprising a mouse IgG-kappa signal sequence, residues 1-153
XX of human BAFF-R and a human IgG Fc sequence.
XX
XX Sequence 302 AA;
XX
XX Query Match 41.2%; Score 205; DB 22; Length 302;
XX Best Local Similarity 67.8%; Pred. No. 3.1e-10;
XX Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX 1 CSQNEYFDSLHACIPCOLRCSNTPTLTQRYC-CYFDSL-----LHACPCLRCSP 53
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 31 CSQNEYFDSLHACIPCOLRCSNTPTLTQRYC-CYFDSL-----LHACPCLRCSP 87
XX
XX RESULT 3

```

AAE15488
 ID AAE15488 standard; Protein; 283 AA.
 AC AAE15488;
 XX
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human BCMA-immunoglobulin Fc region fusion protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 PI Theill LE, Yu G;
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 10B; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein.
 XX
 SQ Sequence 283 AA;
 Query Match 40.5%; Score 201.5; DB 23; Length 283;
 Best Local Similarity 60.6%; Pred. No. 5.8e-10;
 Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
 1 CSQNYFDSLLHACIPQLRCSSNTPTLTCQRYC-CEYFDSL-----LHACPC 47
 5 CSQNYFDSLLHACIPQLRCSSNTPTLTCQRYCNASVTNSVKGNTAGGGGDKHTCP- 63

QY 48 LRCSP 53
 DB 64 -PCPAP 68
 RESULT 4
 AAE15486
 ID AAE15486 standard; peptide; 34 AA.
 XX
 AC AAE15486;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 PI Theill LE, Yu G;
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Claim 1; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein cysteine-rich consensus region.
 XX
 SQ Sequence 34 AA;
 Query Match 40.4%; Score 201; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 34
 Db 1 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 5
 AAE15485
 ID AAE15485 standard; peptide; 51 AA.
 AC AAE15485;
 XX
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B-cell maturation (BCMA) protein extracellular domain.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Claim 1; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC Crohn's disease, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein extracellular domain.
 XX
 SQ Sequence "51 AA;

Query Match 40.4%; Score 201; DB 23; Length 51;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 34
 Db 5 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 6
 AAE15501
 ID AAE15501 standard; peptide; 58 AA.
 AC AAE15501;
 XX
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B cell maturation protein cysteine rich extracellular region.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 13; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC Crohn's disease, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region.

SQ Sequence 58 AA;
 Query Match 40.4%; Score 201; DB 23; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLCQRYC 34
 |||||
 Db 1 CSQNEYFDSLHACIPQCLRCSSNTPTLCQRYC 34

RESULT 7
 AA015484
 ID AA015484 standard; Protein; 181 AA.
 AC AA015484;
 DT 12-MAR-2002 (first entry)
 DE Human B-cell maturation (BCMA) protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 5..38
 FT /note= "Cysteine-rich consensus region; This is region
 FT is specifically claimed as SEQ ID NO: 7 in claim 1 of
 FT the specification"
 FT 52..72
 FT /label= Transmembrane_domain
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 PS Disclosure; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1

CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 XX is human BCMA protein.
 SQ Sequence 181 AA;
 Query Match 40.4%; Score 201; DB 23; Length 181;
 Best Local Similarity 100.0%; Pred. No. 4.3e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLCQRYC 34
 |||||
 Db 5 CSQNEYFDSLHACIPQCLRCSSNTPTLCQRYC 38

RESULT 8
 AA08843
 ID AA08843 standard; peptide; 184 AA.
 AC AA08843;
 XX
 DT 02-JAN-2001 (first entry)
 DE Amino acid sequence of human.
 XX
 KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 57..77
 FT /note= "putative transmembrane domain"
 XX
 PN WO200050633-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-US04925.
 XX
 PR 24-FEB-1999; 99US-0121485.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Ting A;
 XX
 DR WPI; 2000-558405/51.
 XX
 PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression
 XX
 PS Claim 32; Fig 7A; 53pp; English.
 XX
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)-kB activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are

CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing.

XX Sequence 184 AA;
 SQ Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 9
 AAY94001
 ID AAY94001 standard; Protein; 184 AA.

XX AAY94001;

XX 20-OCT-2000 (first entry)

XX A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO200040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US00396.

XX 07-JAN-1999; 99US-0226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58559.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 XX antagonists

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity

CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, and stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.

SQ Sequence 184 AA;

Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 10
 AAE09241

ID AAE09241 standard; Protein; 184 AA.

XX AAE09241;

XX 19-NOV-2001 (first entry)

XX Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US32378.

XX 16-FEB-2000; 2000US-0182938.

XX 22-AUG-2000; 2000US-0226986.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;

XX WPI; 2001-541628/60.

XX N-PSDB; AAD15902.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists

XX Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TACI or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,

CC psoriasis and lupus erythematosus. The present sequence is human
 CC BCMA protein.

XX SQ Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 11

AAE00506
 ID AAE00506 standard; Protein; 184 AA.

XX AC AAE00506;

XX DT 31-JUL-2001 (first entry)

XX DE Human B cell maturation protein (BCMA).

XX KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;
 KW tumour necrosis factor; BCMA; B cell maturation protein.

XX OS Homo sapiens.

XX PN WO200124811-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27579.

XX PR 06-OCT-1999; 99US-0157933.

XX PR 11-FEB-2000; 2000US-0181807.

XX PR 30-JUN-2000; 2000US-0215688.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTEC R & D SA.

XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

XX DR WPI; 2001-266242/27.

XX DR N-PSDB; AAD03844.

XX PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor
 PT (APRIL-R) antagonist

XX PS Claim 3; Fig 3A; 85pp; English.

XX CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or
 CC carcinoma. The method involves administering a composition comprising
 CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or

CC altering an immune response involving a signalling pathway between
 CC APRIL-R and its ligand, APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is human APRIL-R also referred as BCMA or
 CC BCM protein.

XX SQ Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 12

AAE06098

ID AAE06098 standard; Protein; 184 AA.

XX AC AAE06098;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R).

XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour.

XX OS Homo sapiens.

XX PN WO200112812-A2.

XX PD 22-FEB-2001.

XX PF 16-AUG-2000; 2000WO-US22507.

XX PR 17-AUG-1999; 99US-0149378.

XX PR 11-FEB-2000; 2000US-0181684.

XX PR 18-FEB-2000; 2000US-0183536.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTEC R & D SA.

XX PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

XX DR WPI; 2001-202866/20.

XX DR N-PSDB; AAF59998.

XX PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog

XX PS Claim 20; Fig 1; 59pp; English.

XX CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative

disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R.

Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. NO. 4.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||
DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 13

AA71979
ID AA71979 standard; Protein; 184 AA.

XX AC AA71979;

XX DT 28-MAR-2001 (first entry)

XX DE Human B cell maturation factor (BCMA) protein.

XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
XX KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA;
XX KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Domain 1..62
XX FT /label= Extracellular_domain

XX PN WO200068378-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12266.

XX PR 06-MAY-1999; 98US-0132892.

XX PR 01-MAY-2000; 2000US-0201012.

XX PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX PI Shu HS;

XX DR WPI; 2001-016094/02.

XX DR N-PSDB; AAD02125.

XX PT Isolated TALL-1 protein is used to identify compounds that regulate B
XX PT lymphocyte proliferation, used to treat B lymphocyte associated
XX PT autoimmune disorders -

XX PS Claim 37; Page 104-105; 112pp; English.

XX CC The present invention relates to Tumour necrosis factor (TNF) and

CC Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid
CC molecules, proteins (including homologues), and their antibodies. The
CC interaction in particular relates to methods for regulating the
CC maturation between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC mediated immune responses. TALL-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis, or polyarthritis nodosa.
CC The TALL-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.
CC The present sequence is a human B cell maturation factor (BCMA)
CC protein. It is the receptor for TALL-1 protein. BCMA gene is
CC located on chromosome 16. In human tissues, BCMA is expressed by
CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
CC lymphocyte stage but its expression increases with B lymphocyte
CC maturation.
XX SQ Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. NO. 4.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||
DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 14

AAE28961

ID AAE28961 standard; Protein; 184 AA.

XX AC AAE28961;

XX DT 27-JAN-2003 (first entry)

XX DE Human B-cell maturation antigen (BCMA).

XX KW Human; tumour; B-cell maturation antigen; transmembrane activator;
XX KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
XX KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
XX KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
XX KW BCMA; multiple myeloma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 1..48
XX FT /note= "Extracellular domain"

XX FT Region 1..54
XX FT /note= "Antigenic epitope"

XX FT Region 8..41
XX FT /note= "Cysteine rich region"

XX PN WO200266516-A2.

XX PD 29-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US03500.

XX PR 20-FEB-2001; 2001US-270274P.

XX PR 12-APR-2001; 2001US-283447P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kindsvogel W;

XX CC

DR WPI; 2002-723183/79.
DR N-PSDB; AAD46410.
XX
PT B-cell maturation antigen and transmembrane activator and
PT calcium-modulator and cyclophilin ligand-interactor, useful for
PT treating disorders e.g. inflammation or lymphoma -
XX
PS Disclosure; Page 63; 67pp; English.
XX
CC The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present
CC is human BCMA protein.
XX
SQ Sequence 184 AA;
Query Match 40.4%; Score 201; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQCQLRCSSTNPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQCQLRCSSTNPPLTCQRYC 41
RESULT 15
ABP54694
ID ABP54694 standard; Protein; 184 AA.
XX
AC ABP54694;
XX
DT 30-DEC-2002 (first entry)
XX
DE Metastatic colorectal cancer-associated polypeptide.
XX
KW Colorectal cancer; metastasis; differential expression; cytostatic;
KW diagnosis; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200268677-A2.
XX
PD 06-SEP-2002.
XX
PF 14-JAN-2002; 2002WO-US06001.
XX
PR 27-FEB-2001; 2001US-272206P.
PR 02-APR-2001; 2001US-281149P.
PR 17-APR-2001; 2001US-284555P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Mack DH, Markowitz SD;
PI
XX
DR WPI; 2002-698677/75.
DR N-PSDB; ABQ81560.
XX
PT New genes that are up- or down-regulated in colorectal cancer, useful
PT for diagnosing colorectal cancer in a subject, or for identifying
PT modulators of colorectal cancer-associated proteins and genes for
PT treating colorectal cancer -
XX
PS Claim 8; Page 255; 260pp; English.
XX

CC The present sequence is the protein sequence of a human polypeptide
CC encoded by a gene that exhibits decreased expression in colon
CC cancer-derived metastases compared to normal colon tissue. It is
CC an example of claimed polypeptides that are encoded by genes which
CC are differentially expressed in metastatic colorectal cancer cells.
CC Such polypeptides are useful in diagnostic and prognostic assays, for
CC raising antibodies useful e.g. in immunotherapy, and in screening
CC for modulator compounds of therapeutic value.
XX
SQ Sequence 184 AA;
Query Match 40.4%; Score 201; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQCQLRCSSTNPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQCQLRCSSTNPPLTCQRYC 41
Search completed: November 12, 2003, 06:26:09
Job time : 71 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 06:28:28 ; Search time 30 Seconds

(without alignments)
463.723 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEYFDSLHACIPQCLR.....SEYFDSLHACPPATCPQYC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	81	9	US-09-854-864-13
2	230.5	46.3	207	14	US-10-077-438-3
3	230.5	46.3	207	14	US-10-077-137-3
4	205	41.2	302	15	US-10-115-192-12
5	201.5	40.5	283	9	US-09-854-864-9
6	201	40.4	34	9	US-09-854-864-7
7	201	40.4	51	9	US-09-854-864-6
8	201	40.4	58	9	US-09-854-864-21
9	201	40.4	181	9	US-09-854-864-5
10	201	40.4	184	12	US-10-216-074-11
11	201	40.4	184	14	US-10-077-438-1
12	201	40.4	184	14	US-10-077-438-7
13	201	40.4	184	14	US-10-077-137-1
14	201	40.4	184	14	US-10-077-137-7
15	201	40.4	184	15	US-10-068-725-2

16	201	40.4	184	15	US-10-151-882-47
17	201	40.4	184	15	US-10-115-192-8
18	201	40.4	184	15	US-10-008-063-7
19	201	40.4	184	15	US-10-152-363A-27
20	153	30.7	117	9	US-09-854-864-12
21	139.5	28.0	281	9	US-09-854-864-10
22	136	27.3	185	9	US-09-854-864-11
23	136	27.3	185	12	US-10-216-074-17
24	124	24.9	42	12	US-10-145-206-137
25	114	22.9	344	15	US-10-152-363A-52
26	106	21.3	332	15	US-10-152-363A-62
27	106	21.3	348	15	US-10-152-363A-54
28	105	21.1	67	9	US-09-854-864-16
29	99.5	20.0	357	15	US-10-152-363A-56
30	98	19.7	375	12	US-10-029-386-32138
31	98	19.7	401	12	US-10-029-386-33904
32	93	18.7	166	9	US-09-854-864-15
33	93	18.7	166	15	US-10-293-816-6
34	93	18.7	291	10	US-09-779-050A-43
35	93	18.7	293	9	US-09-879-919-22
36	93	18.7	293	9	US-09-854-864-14
37	93	18.7	293	10	US-09-961-376-2
38	93	18.7	293	10	US-09-779-050A-42
39	93	18.7	293	11	US-09-302-863-2
40	93	18.7	293	12	US-09-853-564-2
41	93	18.7	293	12	US-10-268-951-22
42	93	18.7	293	14	US-10-084-971-2
43	93	18.7	293	15	US-10-068-725-4
44	93	18.7	293	15	US-10-151-882-46
45	93	18.7	293	15	US-10-293-816-2

ALIGNMENTS

RESULT 1

US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 498; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 6e+40;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSNTPTTCORYCCYCFDSLHACPLRCSPTCOYCCF 60

Db 1 CSQNEYFDSLHACIPQCLRCSNTPTTCORYCCYCFDSLHACPLRCSPTCOYCCF 60

QY 61 HSEYFDSLHACPPATCPQYC 81

Db 61 HSEYFDSLHACPPATCPQYC 81

RESULT 2

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US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: Immunoregulatory Agent
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match 46.3%; Score 230.5; DB 14; Length 207;
Best Local Similarity 57.8%; Pred. No. 1.9e-14;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCCEYFDSLHAC-PC-LRCSPTCQYC 58
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Db 46 CSQNEYFDSLHACIPCOLRCSSNTPPLTC-----LHACIPCOLRCSSNT---- 90

QY 59 CFHSEYFDSLHACPPATCQPYC 81
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Db 91 -----PPLTCQRYC 99

RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: Immunoregulatory Agent
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
US-09-854-864-9

Query Match 41.2%; Score 205; DB 15; Length 302;
Best Local Similarity 67.8%; Pred. No. 6.5e-12;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC-CEYFDSL-----LHACPCLRCSP 53
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Db 31 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGVDKHTTCP--PCPAP 87

RESULT 5
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
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; ORGANISM: homo sapien
US-10-077-137-3

Query Match 46.3%; Score 230.5; DB 14; Length 207;
Best Local Similarity 57.8%; Pred. No. 1.9e-14;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCCEYFDSLHAC-PC-LRCSPTCQYC 58
|||||
Db 46 CSQNEYFDSLHACIPCOLRCSSNTPPLTC-----LHACIPCOLRCSSNT---- 90

QY 59 CFHSEYFDSLHACPPATCQPYC 81
|||||
Db 91 -----PPLTCQRYC 99

RESULT 4
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match 41.2%; Score 205; DB 15; Length 302;
Best Local Similarity 67.8%; Pred. No. 6.5e-12;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC-CEYFDSL-----LHACPCLRCSP 53
|||||
Db 31 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGVDKHTTCP--PCPAP 87

RESULT 5
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
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Query Match      40.5%; Score 201.5; DB 9; Length 283;
Best Local Similarity 60.6%; Pred. No. 1.3e-11;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC-CREYFDSL-----LHACPC 47
Db 5 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYCNAVSNTSVKGTNAGGGGDKTHTCP- 63

Qy 48 LRCSP 53
Db 64 -PCPAP 68

RESULT 6
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      40.4%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 7
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      40.4%; Score 201; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 8
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      40.4%; Score 201; DB 9; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 9
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      40.4%; Score 201; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 38
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RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match 40.4%; Score 201; DB 12; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 11
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 40.4%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 12
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match 40.4%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1
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7-E371-880-07-50

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 06:24:52 ; Search time 21 Seconds
(without alignments)
163.199 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEYFDSLLHACIPQLR.....SEYFDSLLHACBPATCPQVC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
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5: /cgn2_6/prodata/1/iaa/6C COMB.pcp.*
6: /cgn2_6/prodata/1/iaa/6D COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	40.4	184	4	US-09-854-864-13
2	136	27.3	185	4	US-09-854-864-13
3	93	18.7	166	2	US-08-810-572A-6
4	93	18.7	166	4	US-09-290-333-6
5	93	18.7	166	4	US-09-782-857A-6
6	93	18.7	293	2	US-08-810-572A-2
7	93	18.7	293	4	US-09-290-333-2
8	93	18.7	293	4	US-09-782-857A-2
9	93	18.7	293	4	US-09-879-919-22
10	82	16.5	508	3	US-09-019-095A-8
11	82	16.5	521	3	US-09-019-095A-22
12	82	16.5	526	3	US-09-019-095A-2
13	80	16.1	3075	2	US-08-460-309-5
14	80	16.1	3075	2	US-08-125-077-5
15	80	16.1	5405	3	US-08-718-388-9
16	79	15.9	320	4	US-09-183-861-22
17	79	15.9	320	4	US-09-183-861-55
18	79	15.9	320	4	US-09-022-765-22
19	79	15.9	320	4	US-09-022-765-55
20	79	15.9	320	4	US-09-551-974A-22
21	79	15.9	320	4	US-09-551-974A-55
22	79	15.9	545	3	US-09-019-095A-38
23	78	15.7	109	2	US-08-527-044-2
24	78	15.7	109	3	US-09-013-780-2
25	78	15.7	109	4	US-09-107-532A-4585
26	77.5	15.6	139	3	US-08-965-903B-20
27	77.5	15.6	139	4	US-09-370-398-4

28	77.5	15.6	139	4	US-10-090-190-4	Sequence 4, Appli
29	76.5	15.4	2414	1	US-08-227-536-2	Sequence 2, Appli
30	76.5	15.4	2414	5	PCT-US95-04682-2	Sequence 2, Appli
31	76	15.3	2441	1	US-08-194-468-2	Sequence 2, Appli
32	76	15.3	2441	3	US-08-961-739-2	Sequence 2, Appli
33	76	15.3	2441	4	US-09-514-247A-8	Sequence 8, Appli
34	76	15.3	2441	4	US-09-514-247A-10	Sequence 10, Appli
35	75.5	15.2	156	3	US-08-600-982-30	Sequence 30, Appli
36	75.5	15.2	156	5	PCT-US94-10261A-30	Sequence 30, Appli
37	75.5	15.2	1713	3	US-08-600-982-24	Sequence 24, Appli
38	75.5	15.2	1713	5	PCT-US94-10261A-24	Sequence 24, Appli
39	75	15.1	219	1	US-08-152-019A-31	Sequence 31, Appli
40	75	15.1	219	2	US-08-460-309-18	Sequence 18, Appli
41	75	15.1	219	2	US-08-125-077-18	Sequence 18, Appli
42	75	15.1	430	3	US-08-997-897-2	Sequence 2, Appli
43	75	15.1	430	3	US-09-156-836B-2	Sequence 2, Appli
44	73.5	14.8	339	4	US-09-686-583B-40	Sequence 40, Appli
45	73.5	14.8	381	4	US-09-686-583B-48	Sequence 48, Appli

ALIGNMENTS

RESULT 1
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 40.4%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC 34
Db 8 CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC 41

RESULT 2
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

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Query Match 27.3%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. NO. 4.6e-06;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
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Db 5 CFHSEYFDSLHACKPCHLRGSR--PPATCOPYC 36

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RESULT 3
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

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Query Match	18.7%;	Score 93;	DB 2;	Length 166;
Best Local Similarity	28.4%;	Pred. No. 0.048;		
Matches 21;	Conservative	13;	Mismatches 22;	Indels 18;
				Gaps 5;

Qy	1	CSQNEYFDSLHACIPQLRCSNTPPLTCQRYC---C-----EYFDSLHACPLRCS	51
		: : : : : : : : : : : : : : :	
Db	34	CPEQYWDPLGLGTMSCKTICNHQS-ORTCAAFCSLSCRKEQGFYDHLR--DCISCA	90

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Qy      52  -----PPTCQYCC  59
          |   |   |   |
Db      91  SICGQHPKQCA YFC 104

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RESULT 4
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; ; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
;

Query Match 18.7%; Score 93; DB 4; Length 166;
Best Local Similarity 28.4%; Pred. No. 0.048;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

Qy 1 CSQNEYFDLLHACIPQCLRCSSNPPLTCQRYC-----C-----EYFSLHHACPLRCS 51

Db 34 CPPEQYDPLGLTWCMSCKTICNHQS-ORTCAAFCRSLSCRKEGKFYDHLRL--DCISCA 90

Qy	52	-----PPTCQYCC	59
Db	91	SICGQHPKQCAAYFC	104

RESULT 5
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 18.7%; Score 93; DB 4; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.082;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEYFDSLHACIPQLRCSNTPPLTCORYC-----C-----EYFDSLHACPLRCS 51
Db 34 CPEQYWDPLGLGTCMSCKTICNHQS-ORTCAAFCSRSLSCRKQKGYDHLR--DCISCA 90

QY 52 -----PPTCQYCC 59
Db 91 SICGQHPKQCAVFC 104

RESULT 8
US-09-782-857A-2
Sequence 2, Application US/09782857A
Patent No. 6500428
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 18.7%; Score 93; DB 4; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.082;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEYFDSLHACIPQLRCSNTPPLTCORYC-----C-----EYFDSLHACPLRCS 51
Db 34 CPEQYWDPLGLGTCMSCKTICNHQS-ORTCAAFCSRSLSCRKQKGYDHLR--DCISCA 90

QY 52 -----PPTCQYCC 59
Db 91 SICGQHPKQCAVFC 104

RESULT 9
US-09-879-919-22
Sequence 22, Application US/09879919
Patent No. 6541224
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253PI
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 08/815,783
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 18.7%; Score 93; DB 4; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.082;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEYFDSLHACIPQLRCSNTPPLTCORYC-----C-----EYFDSLHACPLRCS 51
Db 34 CPEQYWDPLGLGTCMSCKTICNHQS-ORTCAAFCSRSLSCRKQKGYDHLR--DCISCA 90

QY 52 -----PPTCQYCC 59
Db 91 SICGQHPKQCAVFC 104

RESULT 10


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/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3075 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;
Best Local Similarity 23.4%; Pred. No. 13;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEYFDSLL--HACIPCQ-----LRCSSNTPLTCQRYCC-- 36
Db 831 CADGYGNFTVPGESVPCDCSGNVDPSEAGHCDVTEGCLKCLGNTDGAHCE--CADGF 889
QY 37 YFDSL-----LHACPC-----LRCSP-PTCQYC--CFHSEYFDSLHACP 73
Db 890 YGDAVTAKNCRACECHVKGSHSAVCHLETGLCDCKENVTGQQCQCLHGYGLDSHGCR 949
QY 74 PATC 77
Db 950 PCNC 953

RESULT 15
US-08-718-388-9
/ Sequence 9, Application US/08718388
/ Patent No. 6271362
/ GENERAL INFORMATION:
/ APPLICANT: MORIKAWA, MINORU
/ APPLICANT: HARADA, NAOKI
/ TITLE OF INVENTION: GENE ENCODING IgG Fc REGION-BINDING
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
/ STREET: PO BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22040-0747
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/718,388
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURPHY JR, GERALD M
/ REGISTRATION NUMBER: 28,977
/ REFERENCE/DOCKET NUMBER: 0230-111
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5405 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-718-388-9

Query Match 16.1%; Score 80; DB 3; Length 5405;
Best Local Similarity 25.4%; Pred. No. 22;
Matches 29; Conservative 12; Mismatches 25; Indels 48; Gaps 10;

QY 1 CSQNEYFDSLLHACI-PCQLRCSNTPLTCQRYCCYFDSLHACPC-----LRCS 51
Db 2733 CPQNSHYE----LCADTCSLGCSSALSAPLQCPDCAE-----GCQCDSGFLYNGQCV 2781
QY 52 PPTCQYC-CFHS-EYFD---SL-----HACPPA-TCQP 79
Db 2782 P--IQCGCYHNGAYEPEQTVLIDNCRQOCTCHAGKVVCQEHSCKFGQVCQP 2833
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/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3075 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;
Best Local Similarity 23.4%; Pred. No. 13;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEYFDSLL--HACIPCQ-----LRCSSNTPLTCQRYCC-- 36
Db 831 CADGYGNFTVPGESVPCDCSGNVDPSEAGHCDVTEGCLKCLGNTDGAHCE--CADGF 889
QY 37 YFDSL-----LHACPC-----LRCSP-PTCQYC--CFHSEYFDSLHACP 73
Db 890 YGDAVTAKNCRACECHVKGSHSAVCHLETGLCDCKENVTGQQCQCLHGYGLDSHGCR 949
QY 74 PATC 77
Db 950 PCNC 953

RESULT 14
US-08-125-077-5
/ Sequence 5, Application US/08125077
/ Patent No. 5872231
/ Patent No. 5872231
/ GENERAL INFORMATION:
/ APPLICANT: Engvall, Eva
/ APPLICANT: Leivo, Ilmo
/ TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
/ TITLE OF INVENTION: Fragments and Uses Thereof
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/125,077
/ FILING DATE: 22-SEP-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US PCT/US 94/10730
/ FILING DATE: 21-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/472,319
/ FILING DATE: 30-JAN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/919,951
/ FILING DATE: 27-JUL-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LA 9721
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3075 amino acids
/ TYPE: amino acid
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Wed Nov 12 06:41:51 2003

us-09-854-864-13.rai

Page 7

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Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 06:21:42 ; Search time 42 Seconds
(without alignments)
185.468 Million cell updates/sec

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Perfect score: 498
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	94.5	19.0	223	2	S38346
3	94.5	19.0	230	2	A38346
4	92.5	18.6	169	1	S18946
5	91.5	18.4	186	2	A45910
6	89	17.9	1574	2	T13954
7	87	17.5	1680	2	A43434
8	86.5	17.4	1548	2	S34583
9	86	17.3	188	2	J6547
10	83	16.7	131	1	K8SHA3
11	83	16.7	175	2	S37649
12	82	16.5	126	2	I46489
13	82	16.5	526	2	J66133
14	81	16.3	2823	2	T23064
15	81	16.3	2823	2	F87908
16	81	16.3	3102	2	T43291
17	80.5	16.2	151	2	S60314
18	80.5	16.2	937	2	I63282
19	80.5	16.2	1101	2	T16840
20	80.5	16.2	1798	2	S53869
21	80	16.1	3075	2	S14458
22	79.5	16.0	965	2	S62935
23	79.5	16.0	1077	2	T41146
24	79.5	16.0	3133	2	S52093
25	79	15.9	861	2	A48825
26	78.5	15.8	201	2	D71190
27	78.5	15.8	294	2	T23682
28	78	15.7	572	2	T29880
29	78	15.7	1188	2	D86236

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCMA protein; BEL protein
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C:Accession: S43486; S31208; S36661
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A>Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bid.
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LA>
A:Cross-references: EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471245
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis
EMBO J. 11, 3897-3904, 1992
A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA>
A:Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A:Accession: S36661
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-184 <LA>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 4/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match 40.4%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 9e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDLSLLHACIPQLRCSNTPTTCQRYC 34
|||||
DB 8 CSQNEFYDLSLLHACIPQLRCSNTPTTCQRYC 41

RESULT 2

B38346
ultra-high-sulfur keratin 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C:Accession: A38660; B38346
R:Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogeli, G.

keratin high-sulfu
high-sulfur kerati
high-sulfur wool m
keratin high-sulfu
zonadhesin - mouse
PACB4A - mouse lfr
hypothetical prote
transcription adap
high-sulfur wool m
high-sulfur wool m
furin (EC 3.4.21.7
transcription coac
CREB-binding prote
ocogelin - mouse
hypothetical prote
adhesive ligand ep

30 77.5 15.6 132 1 KRG73J
31 77.5 15.6 177 2 S37650
32 77 15.5 162 2 I47107
33 77 15.5 172 1 KRSHHA
34 77 15.5 3376 2 T42215
35 76.5 15.4 932 2 I52527
36 76.5 15.4 1513 2 T23681
37 76.5 15.4 2414 2 A54277
38 76 15.3 172 2 I47106
39 76 15.3 182 2 I47105
40 76 15.3 1299 2 T43251
41 76 15.3 2440 2 S39162
42 76 15.3 2441 2 S39161
43 76 15.3 2910 2 T42214
44 75.5 15.2 654 2 T30136
45 75.5 15.2 1713 2 A55347

```

A;Reference number: S18946
A;Accession: S18946
A;Molecule type: mRNA
A;Residues: 1-169 <DRA>
A;Cross-references: EMBL:X63755; NID:G32471; PIDN:CAA45283.1; PID:G32472
R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the
A;Reference number: A36686; MUID:91115951; PMID:1703541
A;Accession: B36686
A;Molecule type: DNA
A;Residues: 1-39, 'Y', 41-169 <MAC>
A;Cross-references: GB:X55293; NID:G34078; PIDN:CAA39005.1; PID:G34079
C;Genetics:
A;Gene: GDB:KRN1
A;Cross-references: GDB:125257; OMIM:148021
A;Map position: 11q13-11q13
C;Superfamily: ultra-high-sulfur keratin
C;Keywords: hair; tandem repeat
F;7-15/Region: Ser-rich nonapeptide repeat
F;59-68/Region: Gly-rich decapeptide repeat
F;69-78/Region: Gly-rich decapeptide repeat
F;79-88/Region: Cys-rich decapeptide repeat
F;89-97/Region: Ser-rich nonapeptide repeat
F;98-107/Region: Cys-rich decapeptide repeat
F;108-117/Region: Cys-rich decapeptide repeat
F;118-126/Region: Ser-rich nonapeptide repeat
F;127-136/Region: Cys-rich decapeptide repeat
F;137-145/Region: Ser-rich nonapeptide repeat
F;146-155/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat

Query Match 18.6%; Score 92.5; DB 1; Length 169;
Best Local Similarity 30.0%; Pred. No. 0,19;
Matches 27; Conservative 5; Mismatches 37; Indels 21; Gaps 5;

Qy 1 CSONEYFDLLHACTPCQLRCSSTPPTTCQRYCCYEYFDLLHAC-PCLR-----CS 51
Db 77 CSQ-----CSCCKPC---CCSSGGSSCCQCKPCSCQCKPCCCSSSGSSCCQ 127
Qy 52 PPTCQYCCFHFSEYFDLLHACPPATCQPYC 81
Db 128 SSCCKPCCSSSGSS---CCQSSCKPCC 154

RESULT 5
A45910
ultra-high-sulfur keratin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999
C;Accession: A45910
R;McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
J. Invest. Dermatol. 92, 263-266, 1989
A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth
A;Reference number: A45910; MUID:89140394; PMID:2465353
A;Accession: A45910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <MCN>
A;Cross-references: GB:M27685; NID:G341749; PIDN:AAA81560.1; PID:gl066818
C;Superfamily: ultra-high-sulfur keratin

Query Match 18.4%; Score 91.5; DB 2; Length 186;
Best Local Similarity 34.7%; Pred. No. 0,25;
Matches 25; Conservative 4; Mismatches 24; Indels 19; Gaps 6;

Qy 14 CIP-CQLRC--SSNTTPPLTCQRYCCYEYFDLLHAC-PCLRGSPPTCQYCCFHFSEYFDLL 69
Db 85 CQPCQPCSCQSSCCQPRCCSSCCQPC--CRPSCQSSC----- 132
Qy 70 HACPPATCQPYC 81
Db 133 --CRPC-CQFPC 141

```

RESULT 6

MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294
A:Experimental source: strain Prague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 17.9%; Score 89; DB 2; Length 1574;
Best Local Similarity 29.4%; Pred. No. 1.9; Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;
QY 1 CSQNEYFDSLHACIPCOL-----RCSSNTPLT-----CQRYCCEY-----FDSLHACPC 47
Db 966 CSAGAPCAVATGSCI-CPAGRWGPRCAQSCPLTFGLNCSQICTCFENGASCDSVTGQC--- 1022
QY 48 LRCSP-----PTQCYCFHSEYFDSLHACPPA-----TCQPYC 81
Db 1023 -HCAFGWVGPTC-----LQACPPGLYGNKCQHSK 1050

RESULT 7

A43434
Furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:g157461; PID:g157462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBgn0004598
A:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 17.5%; Score 87; DB 2; Length 1680;
Best Local Similarity 25.0%; Pred. No. 2.9; Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;
QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTQ---RYC--CEYFDSLH-----ACP--- 46
Db 1051 CPDGFENSNRNKTVPFCFNCAS-----CQDHYEYTCSDH-HLVMEHKYCSACPLDT 1103
QY 47 -----CLRCSPPTCOYC--CFHSEYF--DSLHACPPA-----TC 77
Db 1104 YETEDNKAFCSTCATNGPTDQDICTRSRYAWQNKCLISCPDGFYADKKRLECMPC 1163
QY 78 QPYC 81
Db 1164 QEGC 1167

RESULT 8

S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6,
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:g1005033; PID:g440374
C:Keywords: hydrolase; serine proteinase

Query Match 17.4%; Score 86.5; DB 2; Length 1548;
Best Local Similarity 22.1%; Pred. No. 3.1; Matches 29; Conservative 6; Mismatches 43; Indels 53; Gaps 3;
QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTQRYCCEYFDSL----- 42
Db 1152 CAAVEYWDGSHRCQPCCHKKCSGSPSDQCYTCPRFTLLNTTCVKECPGYHTDKDS 1211
QY 43 -----HACPCLRCSP-----PTQCYCFHSEYFDSLHACF----- 73
Db 1212 QCVLCHSSCRTCEGPHSMQCLSCRPWFQLGKCLLQCRDGYGESISGRCEKCDKSK 1271
QY 74 -----RATCQ 78
Db 1272 SCRGRPRPTDQ 1282

RESULT 9

JC6547
high sulfur protein B2E - rat
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsu, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high
A:Reference number: JC6547; MUID:98201605; PMID:9524245
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DBJ:AB003753; NID:g3046870; PIDN:BAA5573.1; PID:g3046871
C:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2E
A:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.3%; Score 86; DB 2; Length 188;
Best Local Similarity 22.5%; Pred. No. 0.76; Matches 29; Conservative 10; Mismatches 28; Indels 62; Gaps 7;
QY 1 CSQNEYFDSLHACIP-----COLRCSSNTPLTQ-----R 32
Db 69 CSQS-----CCQSCCQTCSCQTCQNS---SCQTSCTGSGGEGSGATSCVR 118
QY 33 YC---CEYFDSLHACPLRCSPPTC-----YCCFHSEYFDSLHAC 72
Db 119 WCRPDCRVEGTCLPCCVSVCTPTTCCQLHQAQSCCRPSYCGQSCCRPA-----CCCHCC 174
QY 73 PPATCQPYC 81
Db 175 EPSCSKPSC 183

```
RESULT 10
KFSHA3
keratin high-sulfur matrix protein IIIA3 - sheep
N:Alternate names: M2.6 protein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996
C:Accession: A02840
R:Swart, L.S.; Haylett, T.
Biochem. J. 133, 641-654, 1973
A:Title: Studies on the high-sulphur proteins of reduced merino wool. Amino acid sequence
A:Reference number: A30269; MUID:74022242; PMID:4584026
A:Accession: A02840
A:Molecule type: protein
A:Residues: 1-131 <SWA>
A:Experimental source: Merino wool
C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: duplication; hair

Query Match          16.7%; Score 83; DB 1; Length 131;
Best Local Similarity 25.2%; Pred. No. 1.1;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

QY 1 CSQNEYFDSLHACIPCOLR-----CSNTPTPLT-----COR-VYCEYFDSLHA 44
Db 18 CLQPYRYD-----PCCCRPVSCQTVGRPVTFVTRPTCEPRPVCDPCSLQSGC 71
QY 45 CPCLRCSPPTCOY-----CCFHSEYFDSLHACP---PATCQP 79
Db 72 CRPTTCPTSCQAVVCRPCWATTCQPVQVQPCPCRTSCQP 114

RESULT 11
S37649
high-sulfur keratin - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S37649
R:Zhunabava, B.D.; Genig, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A:Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A:Reference number: S37649
A:Accession: S37649
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <ZHU>
A:Cross-references: EMBL:X63338; NID:g311881; PIDN:CAA44938.1; PID:g311882
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match          16.7%; Score 83; DB 2; Length 175;
Best Local Similarity 32.4%; Pred. No. 1.3;
Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 5;

QY 17 CQLRCSSNTPTLCQRYCEYFDSLHACPLRCSPPTCO--YCCF-HSEYFDSLHACP 73
Db 25 CQPSCEFS---CCQPSCE-----TSC-----CQPSCCQTSFCDFLASQLVDLQLSCCQ 71
QY 74 PATCQPYC 81
Db 72 PSCCETSC 79

RESULT 12
I46489
cysteine-rich hair keratin associated protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C:Accession: I46489; S49201
R:Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A:Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A:Reference number: I46489; MUID:95228955; PMID:7536172
A:Accession: I46489
```

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-126 <POW>

A:Cross-references: EMBL:X80035; NID:G510540; PIDN:CAA56339.1; PID:G510541

C:Genetics:

A:Gene: KAP4L

C:Superfamily: ultra-high-sulfur keratin

Query Match 16.5%; Score 82; DB 2; Length 126;

Best Local Similarity 30.3%; Pred. No. 1.3;

Matches 23; Conservative 6; Mismatches 23; Indels 24; Gaps 6;

QY 14 CIP--CQLRCSSNTPTLCQRYCEYFDSLHACPLRCSPPTCO-----YCCFHSEYF 65

Db 26 CRPCCRPQCCQ---PSCCRPTCC-----ISSC-----CRPCCQSVCCQPTCCRPSCYI 72

QY 66 DSSLHACPPATCQPYC 81

Db 73 SS---CCRPTCCRPTC 85

RESULT 13

JC6133

deubiquitinating enzyme - mouse

N:Alternate names: DUB-1 protein

C:Species: Mus musculus (house mouse)

C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999

C:Accession: JC6133

R:Zhu, Y.; Carroll, M.; Papa, F.R.; Hochstrasser, M.; D'Andrea, A.D.

Proc. Natl. Acad. Sci. U.S.A. 93, 3275-3279, 1996

A:Title: DUB-1, a deubiquitinating enzyme with growth-suppressing activity.

A:Reference number: JC6133; MUID:96194957; PMID:8622927

A:Accession: JC6133

A:Molecule type: mRNA

A:Residues: 1-526 <ZHU>

A:Cross-references: GB:U41636; NID:g1302629; PIDN:AAC52532.1; PID:g1302630

C:Comment: This enzyme is the first enzyme of the ubiquitin system directly implicated in cell cycle progression, and in cytokine-induced cell proliferation.

C:Genetics:

A:Gene: dub-1

Query Match

Best Local Similarity 16.5%; Score 82; DB 2; Length 526;

Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSNTPTPTLCQRYCEYFDSLHACPLRCSPPTCOYCCFHSEYFDSLHA 71

Db 66 LQCLTHTPPL-----ADYMLSQEHSQTC--CSPEGCKLCAMEALVTQSLHLS 110

RESULT 14

T23064

hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C:Accession: T23064; T25096

R:Barlow, K.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19669

A:Accession: T23064

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2823 <WIL>

A:Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8

A:Experimental source: clone H10E24

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19980

A:Accession: T25096

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2823 <WIL>

A:Cross-references: EMBL:Z81125; PIDN:CAE03385.1; GSPDB:GN00019; CESP:T22A3.8

A:Experimental source: clone T22A3
C:Genetics:
A:Gene: CESP:T22A3.8
A:Map position: 1
A:Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like H

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

QY 1 CSQNEYFDSLHACIPQLRCSNTPL-----TCQRYCCYFDSLHACPLRC-----SPP 53
Db 873 CSDGFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKIGHTTGD 920

QY 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGA VNPQC 953

RESULT 15
F87908
protein T22A3.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C:Accession: F87908; E87908
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <STO>
A:Cross-references: GB:chr_I; PIDN:CAAI5432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A3.8
A:Accession: E87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <ST2>
A:Cross-references: GB:chr_I; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
C:Genetics:
A:Gene: T22A3.8
A:Map position: 1
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like H

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

QY 1 CSQNEYFDSLHACIPQLRCSNTPL-----TCQRYCCYFDSLHACPLRC-----SPP 53
Db 873 CSDGFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKIGHTTGD 920

QY 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGA VNPQC 953

Search completed: November 12, 2003, 06:29:17
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 06:14:12 ; Search time 36 Seconds
(without alignments)
105.810 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEYPDSLHACIPCOLR.....SEYFDSLHACPPATCQPYC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	40.4	184	1	TR17_HUMAN
2	136	27.3	185	1	TR17_MOUSE
3	98	19.7	249	1	T13X_MOUSE
4	93	18.7	293	1	T13X_HUMAN
5	92.5	18.6	169	1	KXUA_HUMAN
6	91	18.3	194	1	KXUB_HUMAN
7	87	17.5	1679	1	FUR2_DROME
8	86.5	17.4	1877	1	PKC5_MOUSE
9	83	16.7	131	1	KRA3_SHEEP
10	82	16.5	526	1	URPW_MOUSE
11	81	16.3	1587	1	LMG3_HUMAN
12	80.5	16.2	937	1	PAC4_RAT
13	80.5	16.2	1798	1	LMB2_HUMAN
14	80	16.1	3075	1	LMN1_HUMAN
15	79.5	16.0	145	1	MCS_RAT
16	79.5	16.0	965	1	YNC3_YEAST
17	79.5	16.0	3133	1	HNCT_BONMO
18	79	15.9	1696	1	PKC5_BRACL
19	77.5	15.6	132	1	KRA3_CAPHI
20	77.5	15.6	139	1	SPY1_HUMAN
21	77	15.5	171	1	KR2A_SHEEP
22	77	15.5	5376	1	ZAN_MOUSE
23	76.5	15.4	2414	1	P300_HUMAN
24	76	15.3	2441	1	CBP_MOUSE
25	75.5	15.2	1713	1	LMN3_HUMAN
26	75	15.1	1581	1	LMG3_MOUSE
27	75	15.1	1609	1	LMG1_HUMAN
28	74.5	15.0	610	1	CABP_BOVIN
29	74	14.9	1786	1	LMB1_HUMAN
30	74	14.9	2442	1	CBP_HUMAN
31	73.5	14.8	313	1	SPY1_MOUSE
32	73.5	14.8	1799	1	LMB2_MOUSE
33	73	14.7	689	1	MEA_ARATH

ALIGNMENTS

RESULT 1

ID	TR17_HUMAN	STANDARD;	PRT;	184 AA.
AC	Q02223;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).			
DE	maturation protein).			
GN	TNFRSF17 OR BCMA OR BCM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.			
RC	TISSUE=Lymph node, and Peripheral blood leukocytes;			
RX	MEDLINE=93010384; PubMed=1396583;			
RA	Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,			
RA	Larsen C.J., Tsapis A.;			
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene			
RT	by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma."			
RL	EMBO J. 11:3897-3904 (1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94218235; PubMed=8165126;			
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"The BCMA gene, preferentially expressed during B lymphoid			
RT	maturation, is bidirectionally transcribed."			
RL	Nucleic Acids Res. 22:1147-1154 (1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99425270; PubMed=10493829;			
RA	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,			
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,			
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,			
RA	Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from			
RT	human chromosome 16p and 16q."			
RL	Genomics 60:295-308 (1999).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.			
RX	MEDLINE=21419161; PubMed=11528522;			
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;			
RT	"Presence of four major haplotypes in human BCMA gene: lack of			
RT	association with systemic lupus erythematosus and rheumatoid			
RT	arthritis."			
RL	Genes Immun. 2:276-279 (2001).			
RN	[5]			
RP	FUNCTION, AND INTERACTION WITH TRAF1 AND TRAF3.			
RX	MEDLINE=20363816; PubMed=10903733;			
RA	Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,			
RA	Inoue J.-I., Devergne O., Tsapis A.;			
RT	"TNF receptor family member BCMA (B cell maturation) associates with			
RT	TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and			
RT	activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38			

34	72.5	14.6	870	1	SRC2_HUMAN	Q96gp6 homo sapien
35	72.5	14.6	969	1	PAC4_HUMAN	P29122 homo sapien
36	72.5	14.6	1592	1	SORL1_CHICK	Q98930 g sortilin-
37	72.5	14.6	1918	1	KEO4_HUMAN	Q9p2e3 homo sapien
38	72	14.5	575	1	TRBM_HUMAN	P07204 homo sapien
39	72	14.5	867	1	SSPO_BOVIN	P98167 bos taurus
40	72	14.5	1367	1	IGIR_HUMAN	P08069 homo sapien
41	72	14.5	1700	1	BAR3_CHITE	Q03376 chironomus
42	72	14.5	3333	1	LMN3_MOUSE	Q61789 mus musculu
43	72	14.5	4655	1	LRP2_HUMAN	P98164 homo sapien
44	71.5	14.4	773	1	MES2_CABEL	O17514 caenorhabdi
45	71.5	14.4	1435	1	BBAL_PLAFC	P19214 plasmodium

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.;
 RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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 DR EMBL; Z14954; CRA78679.1; -
 DR EMBL; Z29575; CRA82691.1; -
 DR EMBL; Z29574; CRA82690.1; -
 DR EMBL; U95742; AAB67251.1; -
 DR EMBL; AB052772; BAB60895.1; -
 DR PIR; S43486; S43486.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0007145; P:signal transduction; TAS.
 KW Receptor; immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 FT DOMAIN 1 54
 FT FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 78 184
 FT REPEAT 7 41
 FT SITE 3 4
 FT BREAKPOINT FOR TRANSLOCATION TO FORM
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT DISULFID, 8 21
 FT BY SIMILARITY.

FT DISULFID 24 37 BY SIMILARITY.
 FT DISULFID 28 41 BY SIMILARITY.
 FT VARIANT 153 153 A -> T.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;
 /FTID=VAR_012234.
 Query Match 40.4%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQQLRCSSNTPLTCORYC 34
 |||||
 DB 8 CSQNEYFDSLHACIPQQLRCSSNTPLTCORYC 41
 RESULT 2
 TR17 MOUSE
 ID _TR17 MOUSE STANDARD; PRT; 185 AA.
 AC O88472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;


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Query Match          19.7%; Score 98; DB 1; Length 249;
Best Local Similarity 25.6%; Pred. No. 0.0044;
Matches 23; Conservative 12; Mismatches 27; Indels 28; Gaps 4;

QY 1 CSQNEFDSLHACIPCOLRCSNTPLTCQRYCCEYFDSLHACPLRCSPTQYCCF 60
Db 6 CPKQYWDSSRKSVCSCALTCQSORS-----QRTCTDF-----CKFNCRKE----- 46

QY 61 HSEYFDSLHAC-----PPATCQPYC 81
Db 47 QGRYYDHLGACVSCDSTCTQHPQCAHFC 76

RESULT 4
T13X_HUMAN
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interact).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RA MEDLINE=97458245; PubMed=9311921;
RX von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz B., Dimke D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RA "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RA high affinity receptor for TNF family members APRIL and BlyS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA
```

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RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP INTERACTION WITH TRAF2 AND TRAF5.
RX MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC -----
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CC -----
CC EMBL; AF023614; AAC51790.1; -
CC EMBL; BC028072; AAH28072.1; -
CC Genew; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004872; F: receptor activity; TAS.
CC GO; GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.
CC InterPro; IPR001368; TNFR C6.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC Receptor; Immune response; Signal anchor; Transmembrane; Glycoprotein;
CC Repeat.
CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC (POTENTIAL).
CC DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
CC REPEAT 33 67 TNFR-CYS 1.
CC REPEAT 70 104 TNFR-CYS 2.
CC DISULFID 34 47 BY SIMILARITY.
CC DISULFID 50 62 BY SIMILARITY.
CC DISULFID 54 66 BY SIMILARITY.
CC DISULFID 71 86 BY SIMILARITY.
CC DISULFID 89 100 BY SIMILARITY.
CC DISULFID 93 104 BY SIMILARITY.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 251 251 P -> L (IN REF. 2).
CC SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
Query Match 18.7%; Score 93; DB 1; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.016;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEFDSLHACIPCOLRCSNTPLTCQRYC-----C-----EYFDSLHACPLRCS 51
Db 34 CPBEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCSLRSCKEQGFYDHLR--DCISCA 90
FUNCTION.
```


DE Furin-like protease 2 precursor (BC 3.4.21.75) (Furin 2).
GN FUR2 OR CG18734/CG4235.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R, Tuebingen, and Iso-1;
RX MEDLINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RT Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.,
RT "Cloning and functional expression of Dfurin2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RL J. Biol. Chem. 267:17208-17215(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Iso-1;
RX MEDLINE=95186060; PubMed=7880443;
RA Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
RT van de Ven W.J.M.;
RT "The Dfur2 gene of Drosophila melanogaster: genetic organization,
RT expression during embryogenesis, and pro-protein processing activity
RT of its translational product Dfurin2.";
RL DNA Cell Biol. 14:223-234(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: Furin is likely to represent the ubiquitous endoprotease
CC activity within constitutive secretory pathways and capable of
CC cleavage at the RX(K/R)R consensus motif (By similarity).
CC
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their

proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys. Releases albumin,
complement component C3 and von Willebrand factor from their
respective precursors.
-!- TISSUE SPECIFICITY: Transient expression in a subset of central
nervous system neurons during embryonic stages 12-13. Expression
in developing tracheal tree from stage 13 to end of embryonic
development.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8, FURIN SUBFAMILY.

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DR EMBL; M94375; AAA28551.1; -;
DR EMBL; L33831; AAA69860.1; -;
DR EMBL; AE003502; AAF48598.1; -;
DR PIR; A43434; A43434.
DR HSSP; Q99405; 1MPT.
DR MEROPS; S08.049; -;
DR Flybase; FBgn0004598; Fur2.
DR GO; GO:004276; F:furin activity; IDA.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR002884; P:domain.
DR InterPro; IPR000209; Peptidase S8.
DR Pfam; PF01483; P_protein; PARTIAL.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P:domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_HIS; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
KW Multigene family; Zymogen; Repeat.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 1 318
FT CHAIN 319 1679
FT ACT_SITE 417 417
FT ACT_SITE 456 456
FT ACT_SITE 637 637
FT DOMAIN 961 1443
FT REPEAT 961 1006 1.
FT REPEAT 1007 1056 2.
FT REPEAT 1057 1103 3.
FT REPEAT 1104 1152 4.
FT REPEAT 1153 1204 5.
FT REPEAT 1205 1253 6.
FT REPEAT 1254 1298 7.
FT REPEAT 1299 1345 8.
FT REPEAT 1346 1392 9.
FT REPEAT 1393 1443 10.
FT TRANSMEM 1512 1532
FT DOMAIN 1533 1679
FT CARBOHYD 3 3
FT CARBOHYD 109 109
FT CARBOHYD 130 130
FT CARBOHYD 205 205
FT CARBOHYD 442 442
FT CARBOHYD 480 480
FT CARBOHYD 927 927
FT CARBOHYD 1060 1060
FT CARBOHYD 1181 1181
FT CARBOHYD 1274 1274
FT CARBOHYD 1277 1277
FT CARBOHYD 1439 1439
FT CONFLICT 152 153
FT CONFLICT 177 177
FT CONFLICT 213 213
V -> F (IN REF. 1).
V -> VDOL (IN REF. 1).

SQ SEQUENCE 1679 AA; 183369 MW; 3F9E749F0B021CF6 CRC64;
 Query Match 17.58; Score 87; DB 1; Length 1679;
 Best Local Similarity 25.08; Pred.No. 0.33;
 Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;

 QY 1 CSQNEYPDSLHACIPQCLRCSSNTPLTQ---RYC---CEYFDSLH-----ACP--- 46
 Db 1050 CPDGYPENSNRCTVCPCEPCAS-----CQDPEYCTSCDH-HLVNHEHKCVSACP LDT 1102
 QY 47 -----CLRCSPTQCYC---CHPSYF--DSLHACPPA-----TC 77
 Db 1103 YETEDNKAFCSTCATCNGFTQDCITCRSSRYAWQNKCLISCPDGFYADKKRLCMPC 1162
 QY 78 QPVC 81
 Db 1163 QEGC 1166

 RESULT 8
 PKC5 MOUSE STANDARD; PRT; 1877 AA.
 ID PKC5 MOUSE
 AC Q04552; Q62040;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protease convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proteinase convertase PC5) (Subtilisin/kexin-like protease PC5)
 DE (Convertase PC5) (PC6) (Subtilisin-like proteinase convertase 6)
 DE (SPC6).
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
 RC STRAIN=ICR; TISSUE=Intestine;
 RX MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform from an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PC5A).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PC5A).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=93342056; PubMed=8341687;
 RA Lusson J., Vicaud J., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PC5 are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION
 RX MEDLINE=96293359; PubMed=8698813;

RA Constam D.B., Calfon M., Robertson E.J.;
 RT "SPCA, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subilisin-like proteinase spc6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 can be any amino acid and Yaa is Arg or Lys.
 CC -!- SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 EARLY ENDOSOMES.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=PC5B; Synonyms=Long;
 IsoID=Q04592-1; Sequences=Displayed;
 Name=PC5A; Synonyms=Short;
 IsoID=Q04592-2; Sequences=VSP 005438, VSP 005439;
 CC -!- TISSUE SPECIFICITY: PC5A IS EXPRESSED IN MOST TISSUES BUT IS MOST
 ABUNDANT IN THE INTESTINE AND ADRENALS. PC5B IS EXPRESSED IN THE
 INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -!- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO.
 EXCEPT IN THE DEVELOPING NERVOUS SYSTEM. THE RIBS AND THE LIVER,
 BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN
 E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
 STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5
 ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 ISOFORM B OCCUR AT E12.5.
 CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
 RETICULUM.
 CC -!- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 WITH THE TGN SORTING PROTEIN PACS-1.
 CC -!- SIMILARITY: Belongs to peptidase family S8.
 CC -!- SIMILARITY: Contains 1 homo B/P domain.
 CC -----
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 CC -----
 CC EMBL; D17583; BAA04507.1; -;
 DR EMBL; D12619; BAA02143.1; -;
 DR EMBL; L14932; AAA74636.1; -;
 DR PIR; A48225; A48225.
 DR PIR; S34583; S34583.
 DR HSP; Q99405; IMPT.
 DR MEROPS; S08.076; -.

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DR EMBL; U41636; AAC52532.1; -
 DR PIR; JC6133; JC6133.
 DR MEROPS; C19.031; -
 DR MGD; MGI:107699; Dub1.
 DR GO; GO:0004843; Fubiquitin-specific protease activity; IDA.
 DR GO; GO:0016579; Fubiquitin deubiquitination; IDA.
 DR InterPro; IPR001394; UCH-2.
 DR Pfam; PF00443; UCH; 1.
 DR PROSITE; PS00973; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS02335; UCH_2_3; 1.

KW Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family.
 FT ACT_SITE 60 60
 FT ACT_SITE 298 298 BY SIMILARITY.
 FT ACT_SITE 307 307 BY SIMILARITY.
 FT MUTAGEN 60 60 C->S; LOSS OF ACTIVITY.
 SQ SEQUENCE 526 AA; 59073 MW; 263AA7B7579694EA CRC64;

Query Match 16.5%; Score 82; DB 1; Length 526;
 Best Local Similarity 35.8%; Pred. No. 0.34;
 Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSSNTPPLTCORYCEYFDSLHACPLRCQCPPTCCVCCFFHSEYFDSLHHA 71
 Db 66 LCLTHTPPL-----ADYMLSQEHSQTC--CSPEGKLCAMEALVTQSLHS 110

RESULT 11

LMG3 HUMAN
 ID LMG3 HUMAN STANDARD; PRT; 1587 AA.
 AC Q9YGN6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).
 GN LAMC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99242614; PubMed=10225960;
 RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
 RA "Characterization and expression of the laminin gamma3 chain: a novel,
 RT non-basement membrane-associated, laminin chain.";
 RL J. Cell Biol. 145:605-618(1999).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
 CC the reproductive tracts.
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -!- DOMAIN: DOMAIN IV IS GLOBULAR.
 CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.

-!- SIMILARITY: Contains 1 laminin IV domain.

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DR EMBL; AF041835; AAD36991.1; -
 DR HSSP; P02468; 1TLE.
 DR Genew; HGNC:6494; LAMC3.
 DR MIM; 604349; -

DR GO; GO:0016020; C-membrane; TAS.
 DR GO; GO:0005198; F:structural molecule activity; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000034; Laminin B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001886; LamNT.

DR Pfam; PF00052; laminin_B; 1.
 DR Pfam; PF00053; laminin_EGF; 9.
 DR Pfam; PF00055; laminin_Nterm; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD002082; Lam_N2; 1.
 DR SMART; SM00180; EGF_Lam; 9.
 DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF_1; 7.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 10.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 1587
 FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 271 326 LAMININ EGF-LIKE 1.
 FT DOMAIN 327 382 LAMININ EGF-LIKE 2.
 FT DOMAIN 383 429 LAMININ EGF-LIKE 3.
 FT DOMAIN 430 479 LAMININ EGF-LIKE 4.
 FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).
 FT DOMAIN 490 672 LAMININ DOMAIN IV.
 FT DOMAIN 673 706 LAMININ EGF-LIKE 5 (C-TERMINAL).
 FT DOMAIN 707 754 LAMININ EGF-LIKE 6.
 FT DOMAIN 755 809 LAMININ EGF-LIKE 7.
 FT DOMAIN 810 865 LAMININ EGF-LIKE 8.
 FT DOMAIN 866 916 LAMININ EGF-LIKE 9.
 FT DOMAIN 917 964 LAMININ EGF-LIKE 10.
 FT DOMAIN 965 1013 LAMININ EGF-LIKE 11.
 FT DOMAIN 1014 1587 DOMAIN II AND I.
 FT DOMAIN 1071 1141 COILED COIL (POTENTIAL).
 FT DOMAIN 1200 1229 COILED COIL (POTENTIAL).
 FT DOMAIN 1424 1504 COILED COIL (POTENTIAL).
 FT DOMAIN 1535 1579 COILED COIL (POTENTIAL).
 FT SITE 1059 1061 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 87 87 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 328 328 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 631 631 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 837 837 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 980 980 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 1185 1185 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 1518 1518 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1587 AA; 172051 MW; 3CB6E09B5F203319 CRC64;

Query Match 16.3%; Score 81; DB 1; Length 1587;
 Best Local Similarity 31.0%; Pred. No. 1.2;
 Matches 22; Conservative 8; Mismatches 31; Indels 10; Gaps 4;

QY 12 HACPQLRCSSNTPPLTCORYCEYFDSLHACPLRC-----SPPTCCVCCFFHSEYFDS 67
 Db 322 HCLUPC--NCSGRSECTFDR---ELFRSTGHGGRCHCHDHTAGPHCQCFYHWD 376

OY 68 LHACPPATCQ 78
 DB 377 RM-PQPCDCQ 386

RESULT 12
 ID_PAC4 RAT STANDARD; PRT; 937 AA.
 AC Q63415;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
 DE (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
 DE convertase 4) (SPC4).
 GN PACE4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Pituitary;
 RA MEDLINE=94349873; PubMed=8070361;
 RA Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
 RT "PACE4: a subtilisin-like endoprotease prevalent in the anterior
 RT pituitary and regulated by thyroid status";
 RL Endocrinology 135:1178-1185(1994).
 CC -!- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTIDASE ACTIVITY WITHIN THE
 CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
 CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
 CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
 CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 CC propeptides by cleavage of Arg-Xaa-Xaa-Arg-|-Zaa bonds, where Xaa
 CC can be any amino acid and Yaa is Arg or Lys.
 CC -!- COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND
 CC IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.
 CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -!- SIMILARITY: Belongs to peptidase family S8.
 CC -!- SIMILARITY: Contains 1 homo B/P domain.
 CC -----
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 CC -----
 DR EMBL; L31894; AAA61987.1; -;
 DR PIR; I53282; I53282.
 DR HSSP; Q99405; 1MPT.
 DR MEROPS; S08.075; -;
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000209; Peptidase_S8.
 DR InterPro; IPR002884; P_domain.
 DR Pfam; PF01483; P_protein; PARTIAL.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU; S.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 DR PROSITE; PS00139; SUBTILASE ASP; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium;
 DE Cleavage on pair of basic residues; Repeat.
 FT SIGNAL 1 45 POTENTIAL.
 FT PROPEP 46 132 POTENTIAL.
 FT CHAIN 133 937 PAIRED BASIC AMINO ACID CLEAVING ENZYME
 FT 4.

FT DOMAIN 133 454 CATALYTIC.
 FT DOMAIN 477 615 HOMO B.
 FT DOMAIN 680 937 CYS-RICH MOTIF (CRM) REGION.
 FT SITE 132 133 CLEAVAGE (AUTO-).
 FT SITE 534 536 CELL ATTACHMENT SITE (POTENTIAL).
 FT ACT_SITE 186 186 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 401 401 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 882 882 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 900 900 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 937 AA; 104053 MW; F3865557C33705C8 CRC64;
 Query Match 16.2%; Score 80.5; DB 1; Length 937;
 Best Local Similarity 24.4%; Pred. No. 0.82;
 Matches 30; Conservative 9; Mismatches 39; Indels 45; Gaps 6;
 OY 1 CSQNEYFDSLHLHACIPCOLRCS-----SNTPTPLTCQ--YCCEYFDSLHACP----- 46
 DB 701 CPLGYFGDTAARCRCHKGCETCTGSRPTQCLSCRRGFVHHQETNTCVLCPAGLYADE 760
 OY 47 ----CLRCSPTTCQYC-----CFHSEYFDSLHLHACPPATCQ 78
 DB 761 SQRCLRCH-PSCKOKVDEPEKSTVCKEGFSLARGSCIPDCEPTYFDSLIRC--GECH 817
 OY 79 PYC 81
 DB 818 HTC 820

RESULT 13
 ID_LMB2_HUMAN STANDARD; PRT; 1798 AA.
 AC P52268; Q16321;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain).
 GN LMB2 OR LAMS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA MEDLINE=95213013; PubMed=7698745;
 RA Wever U.M., Gerscke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
 RA Champliand M.F., Burgess R.E., Albrechtsen R.;
 RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,
 RT chromosomal localization, and expression in carcinomas";
 RL Genomics 24:243-252(1994).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA MEDLINE=95316263; PubMed=7795887;
 RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
 RA Sarioja H., Tryggvason K.;
 RT "The human laminin beta 2 chain (S-laminin): structure, expression in
 RT fetal tissues and chromosomal assignment of the LAMB2 gene";
 RL Matrix Biol. 14:489-497(1995).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC

CC CLEFT OF THE NEUROMUSCULAR JUNCTION.

CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT

CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.

CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.

CC -!- SIMILARITY: Contains 1 laminin IV domain.

CC -----

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CC use by non-profit institutions as long as its content is in no way

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CC -----

DR EMBL; Z68155; CAA92279.1; -

DR EMBL; Z68156; CAA92279.1; JOINED.

DR EMBL; X79683; CAA56130.1; -

DR EMBL; X77512; AAB34682.2; -

DR PIR; S53869; S53869.

DR HSP; P02468; IKLO.

DR Genew; HGNC:6487; LAMB2.

DR MIM; 150325; -

DR GO; GO:0005605; C:basal lamina; TAS.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR001886; LamNT.

DR Pfam; PF00053; laminin_EGF; 13.

DR Pfam; PF00055; laminin_Nterm; 1.

DR PRINTS; PR00011; EGF_LAMININ.

DR SMART; SM00180; EGF_Lam; 13.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF 1; 10.

DR PROSITE; PS01186; EGF 2; 2.

DR PROSITE; PS01248; LAMININ TYPE EGF; 12.

KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1 32

FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.

FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).

FT DOMAIN 283 346 LAMININ EGF-LIKE 1.

FT DOMAIN 347 409 LAMININ EGF-LIKE 2.

FT DOMAIN 410 469 LAMININ EGF-LIKE 3.

FT DOMAIN 470 521 LAMININ EGF-LIKE 4.

FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).

FT DOMAIN 553 781 LAMININ DOMAIN IV.

FT DOMAIN 783 830 LAMININ EGF-LIKE 6.

FT DOMAIN 831 876 LAMININ EGF-LIKE 7.

FT DOMAIN 877 926 LAMININ EGF-LIKE 8.

FT DOMAIN 927 985 LAMININ EGF-LIKE 9.

FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.

FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.

FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.

FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.

FT DOMAIN 1190 1409 DOMAIN II.

FT DOMAIN 1410 1442 DOMAIN ALPHA.

FT DOMAIN 1443 1798 DOMAIN I.

FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).

FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).

FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).

FT DISULFID 283 292 BY SIMILARITY.

FT DISULFID 285 310 BY SIMILARITY.

FT DISULFID 312 324 BY SIMILARITY.

FT DISULFID 324 344 BY SIMILARITY.

FT DISULFID 347 356 BY SIMILARITY.

FT DISULFID 349 374 BY SIMILARITY.

FT DISULFID 377 386 BY SIMILARITY.

FT DISULFID 389 407 BY SIMILARITY.

FT DISULFID 410 423 BY SIMILARITY.

FT DISULFID 412 438 BY SIMILARITY.

FT DISULFID 440 449 BY SIMILARITY.

FT DISULFID 452 467 BY SIMILARITY.

FT DISULFID 470 484 BY SIMILARITY.

FT DISULFID 472 491 BY SIMILARITY.

FT DISULFID 493 502 BY SIMILARITY.

FT DISULFID 505 519 BY SIMILARITY.

FT DISULFID 783 795 BY SIMILARITY.

FT DISULFID 785 802 BY SIMILARITY.

FT DISULFID 804 813 BY SIMILARITY.

FT DISULFID 816 828 BY SIMILARITY.

FT DISULFID 831 843 BY SIMILARITY.

FT DISULFID 833 850 BY SIMILARITY.

FT DISULFID 852 861 BY SIMILARITY.

FT DISULFID 864 874 BY SIMILARITY.

FT DISULFID 877 886 BY SIMILARITY.

FT DISULFID 879 893 BY SIMILARITY.

FT DISULFID 896 905 BY SIMILARITY.

FT DISULFID 908 924 BY SIMILARITY.

FT DISULFID 927 943 BY SIMILARITY.

FT DISULFID 929 954 BY SIMILARITY.

FT DISULFID 956 965 BY SIMILARITY.

FT DISULFID 968 983 BY SIMILARITY.

FT DISULFID 986 1000 BY SIMILARITY.

FT DISULFID 988 1007 BY SIMILARITY.

FT DISULFID 1010 1019 BY SIMILARITY.

FT DISULFID 1022 1035 BY SIMILARITY.

FT DISULFID 1095 1107 BY SIMILARITY.

FT DISULFID 1097 1114 BY SIMILARITY.

FT DISULFID 1116 1125 BY SIMILARITY.

FT DISULFID 1128 1140 BY SIMILARITY.

FT DISULFID 1143 1155 BY SIMILARITY.

FT DISULFID 1145 1162 BY SIMILARITY.

FT DISULFID 1164 1173 BY SIMILARITY.

FT DISULFID 1176 1187 BY SIMILARITY.

FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).

FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).

FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).

FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 914 914 R -> G (IN REF. 2).

FT CONFLICT 1179 1179 G -> A (IN REF. 2).

SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match 16.2%; Score 80.5; DB 1; Length 1798;

Best Local Similarity 26.9%; Pred.No.1.5;

Matches 29; Conservative 7; Mismatches 31; Indels 41; Gaps 8;

QY 1 CSONEYFDSL-----HACIP-----COL-RCSSNTPLTCQRYCC 35

Db 943 CHQDEYSQQIVCHCRAGYGLRCEACAPGHGDFSPRGRCQCECSGNDPMDPD--AC 1000

QY 36 EYFDSLHACPLRC-----SPTCQYC--CFHSEYFDSLHACPPATC 77

Db 1001 D-----PHTGCLRLHHTGPHCAHCKPGHGAARQSCHRC---TC 1040

RESULT 14

LMAL_HUMAN

ID LMAL_HUMAN STANDARD; PRT; 3075 AA.

AC P25391;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Laminin alpha-1 chain precursor (Laminin A chain).

GN LMAL1 OR LAMA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP RX MEDLINE=91333420; PubMed=1714537;
RA Haaparanta T., Uitto J., Ruoslahti E., Engvall E.;
RT "Molecular cloning of the cDNA encoding human laminin A chain.";
RL Matrix 11:151-160(1991).
RN [2]
RP RX SEQUENCE OF 1-2628 FROM N.A.
RA MEDLINE=91264789; PubMed=2049067;
RA Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P.,
RA Tryggvason K.;
RT "Primary structure of the human laminin A chain. Limited expression
RT in human tissues.";
RL Biochem. J. 276:369-379(1991).
RN [3]
RP RX SEQUENCE OF 2397-3072 FROM N.A.
RA MEDLINE=9280632; PubMed=2733383;
RA Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S.,
RA Sanborn D., Sasaki T., Kuivaniemi H., Chu M.L., Deutzmann R.,
RA Timpl R., Uitto J.;
RT "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1
RT and B2 chains, and expression of the corresponding genes in human
RT skin and cultured cells.";
RL Lab. Invest. 60:772-782(1989).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
CC LAMININ-3 (S-LAMININ).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 17 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 2 laminin IV domains.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58531; CAA41418.1; -;
DR PIR; S14458; S14458.
DR HSSP; Q60675; LOUO.
DR GenBank; HGNC:6481; LAM1.
DR MIM; 150320; -;
DR GO; GO:0005606; C:laminin-1; NAS.
DR GO; GO:0005608; C:laminin-3; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
DR GO; GO:0016477; P:cell migration; NAS.
DR GO; GO:0007275; P:development; NAS.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000034; Laminin B.
DR InterPro; IPR002049; Laminin EGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR001886; LamNT.
DR Pfam; PF00052; laminin B; 2.
DR Pfam; PF00053; laminin EGF; 14.
DR Pfam; PF00054; laminin G; 5.
DR Pfam; PF00055; laminin Nterm; 1.
DR PRINTS; BR00011; EGFLAMININ.

DR ProDom; PD002082; Lam_N2; 1.
DR ProDom; PD003031; Laminin_B; 2.
DR SMART; SM00180; EGF Lam; 15.
DR SMART; SM00281; LamB; 2.
DR SMART; SM00282; LamC; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ TYPE EGF; 15.
DR PROSITE; PS50025; LAM G DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 3075 LAMININ ALPHA-1 CHAIN.
FT DOMAIN 18 269 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 270 326 LAMININ EGF-LIKE 1.
FT DOMAIN 327 396 LAMININ EGF-LIKE 2.
FT DOMAIN 397 453 LAMININ EGF-LIKE 3.
FT DOMAIN 454 502 LAMININ EGF-LIKE 4.
FT DOMAIN 503 512 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 517 708 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 709 741 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 742 790 LAMININ EGF-LIKE 6.
FT DOMAIN 791 848 LAMININ EGF-LIKE 7.
FT DOMAIN 849 901 LAMININ EGF-LIKE 8.
FT DOMAIN 902 950 LAMININ EGF-LIKE 9.
FT DOMAIN 951 997 LAMININ EGF-LIKE 10.
FT DOMAIN 998 1043 LAMININ EGF-LIKE 11.
FT DOMAIN 1044 1089 LAMININ EGF-LIKE 12.
FT DOMAIN 1090 1149 LAMININ EGF-LIKE 13.
FT DOMAIN 1150 1159 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT DOMAIN 1160 1361 LAMININ EGF-LIKE 14 (DOMAIN IV A).
FT DOMAIN 1362 1402 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT DOMAIN 1403 1451 LAMININ EGF-LIKE 15.
FT DOMAIN 1452 1508 LAMININ EGF-LIKE 16.
FT DOMAIN 1509 1555 LAMININ EGF-LIKE 17.
FT DOMAIN 1556 2116 DOMAIN II AND I.
FT DOMAIN 2117 2297 LAMININ G-LIKE 1.
FT DOMAIN 2305 2481 LAMININ G-LIKE 2.
FT DOMAIN 2486 2673 LAMININ G-LIKE 3.
FT DOMAIN 2713 2885 LAMININ G-LIKE 4.
FT DOMAIN 2890 3070 LAMININ G-LIKE 5.
FT DOMAIN 1706 1796 COILED COIL (POTENTIAL).
FT DOMAIN 1968 1989 COILED COIL (POTENTIAL).
FT DOMAIN 2088 2120 COILED COIL (POTENTIAL).
FT SITE 2534 2536 CELL ATTACHMENT SITE.
FT DISULFID 270 279 BY SIMILARITY.
FT DISULFID 272 290 BY SIMILARITY.
FT DISULFID 292 301 BY SIMILARITY.
FT DISULFID 297 305 POTENTIAL.
FT DISULFID 304 324 BY SIMILARITY.
FT DISULFID 327 336 BY SIMILARITY.
FT DISULFID 329 361 BY SIMILARITY.
FT DISULFID 364 373 BY SIMILARITY.
FT DISULFID 376 394 BY SIMILARITY.
FT DISULFID 397 409 BY SIMILARITY.
FT DISULFID 399 427 BY SIMILARITY.
FT DISULFID 429 438 BY SIMILARITY.
FT DISULFID 441 451 BY SIMILARITY.
FT DISULFID 454 467 BY SIMILARITY.
FT DISULFID 456 471 BY SIMILARITY.
FT DISULFID 473 482 BY SIMILARITY.
FT DISULFID 485 500 BY SIMILARITY.
FT DISULFID 742 751 BY SIMILARITY.
FT DISULFID 744 757 BY SIMILARITY.
FT DISULFID 760 769 BY SIMILARITY.
FT DISULFID 772 788 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 793 816 BY SIMILARITY.
FT DISULFID 819 828 BY SIMILARITY.
FT DISULFID 831 846 BY SIMILARITY.
FT DISULFID 849 863 BY SIMILARITY.
FT DISULFID 851 870 BY SIMILARITY.

FT DISULFID 873 882 BY SIMILARITY.
 FT DISULFID 885 899 BY SIMILARITY.
 FT DISULFID 902 914 BY SIMILARITY.
 FT DISULFID 904 921 BY SIMILARITY.
 FT DISULFID 923 932 BY SIMILARITY.
 FT DISULFID 935 948 BY SIMILARITY.
 FT DISULFID 951 963 BY SIMILARITY.
 FT DISULFID 953 969 BY SIMILARITY.
 FT DISULFID 971 980 BY SIMILARITY.
 FT DISULFID 983 995 BY SIMILARITY.
 FT DISULFID 998 1007 BY SIMILARITY.
 FT DISULFID 1000 1014 BY SIMILARITY.
 FT DISULFID 1016 1025 BY SIMILARITY.
 FT DISULFID 1028 1041 BY SIMILARITY.
 FT DISULFID 1044 1056 BY SIMILARITY.
 FT DISULFID 1046 1063 BY SIMILARITY.
 FT DISULFID 1065 1074 BY SIMILARITY.
 FT DISULFID 1077 1087 BY SIMILARITY.
 FT DISULFID 1403 1412 BY SIMILARITY.
 FT DISULFID 1405 1419 BY SIMILARITY.
 FT DISULFID 1422 1431 BY SIMILARITY.
 FT DISULFID 1434 1449 BY SIMILARITY.
 FT DISULFID 1452 1466 BY SIMILARITY.
 FT DISULFID 1454 1476 BY SIMILARITY.
 FT DISULFID 1479 1488 BY SIMILARITY.
 FT DISULFID 1491 1506 BY SIMILARITY.
 FT DISULFID 1509 1521 BY SIMILARITY.
 FT DISULFID 1511 1528 BY SIMILARITY.
 FT DISULFID 1530 1539 BY SIMILARITY.
 FT DISULFID 1542 1553 BY SIMILARITY.
 FT DISULFID 1556 1566 INTERCHAIN (PROBABLE).
 FT DISULFID 1560 1560 INTERCHAIN (PROBABLE).
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 555 555 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 665 665 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 763 763 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 926 926 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 952 952 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1407 1407 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1579 1579 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. .) (POTENTIAL).
 Query Match 16.1%; Score 80; DB 1; Length 3075;
 Best Local Similarity 23.4%; Pred. No. 2.9;
 Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;
 QY 1 CSQNEVFDLSL--HACIPQC-----LRCSNTPPLTCQRYCC-- 36
 Db 831 CADGYGNPTVPGESCVPCDCSGNVPSEAGHCDSTVGECLKLGNTDGAHGER-CADGF 889
 QY 37 YFDSL-----LHACPC-----LRCSNTPPLTCQRYCC-- 36
 Db 890 YGDAVTAKNCRACECHVKGSHSAVCHLETGLCDCKENVTGQCDQCLHGYGLDSHGCR 949
 QY 74 PATC 77
 Db 950 PCMC 953

RESULT 15

MCS_RAT ID_MCS_RAT STANDARD; PRT; 145 AA.
 AC Q64298;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm mitochondrial associated cysteine-rich protein.
 GN MCSP OR SNCP OR MCS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RP TISSUE-Testis;
 RC MEDLINE=96231839; PubMed=8634143;
 RX Adham I.M., Tessmann D., Soliman K.A., Murphy D., Kremling H.,
 RA Spitzer C., Engel W.;
 RT "Cloning, expression, and chromosomal localization of the rat
 RT mitochondrial capsule selenoprotein gene (MCS): the reading frame
 RT does not contain potential UGA selenocysteine codons.";
 RL DNA Cell Biol. 15:159-166(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=97073319; PubMed=8916043;
 RA Cataldo L., Baig X., Oke R., Mastrangelo M.A., Kleene K.C.;
 RT "Developmental expression, intracellular localization, and selenium
 RT content of the cysteine-rich protein associated with the
 RT mitochondrial capsules of mouse sperm.";
 RL Mol. Reprod. Dev. 45:320-331(1996).
 CC -!- FUNCTION: Involved in sperm motility. Its absence is associated
 CC with genetic background dependent male infertility. Infertility
 CC may be due to reduced sperm motility in the female reproductive
 CC tract and inability to penetrate the oocyte zona pellucida (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Becomes associated with the
 CC spermatid mitochondrial capsule at step 16 of spermatogenesis (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Testis. Is selectively expressed in the
 CC spermatids of seminiferous tubules.
 CC -!- DEVELOPMENTAL STAGE: Expressed in postmeiotic cells.
 CC -!- CAUTION: Was originally (Ref.1) thought to be a selenoprotein and
 CC was known as sperm mitochondrial capsule selenoprotein.
 CC -----
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 CC -----
 DR EMBL; X87883; CAA61138.1; --
 DR EMBL; U48702; AAB01896.1; --
 DR GO; GO:0005739; C:mitochondrion; ISS.
 DR GO; GO:0030317; P:Sperm motility; ISS.
 KW Fertilization; Mitochondrion.
 SQ SEQUENCE 145 AA; 15148 MW; 5BB70D1ACA86814D CRC64;
 Query Match 16.0%; Score 79.5; DB 1; Length 145;
 Best Local Similarity 32.9%; Pred. No. 0.17;
 Matches 24; Conservative 1; Mismatches 27; Indels 21; Gaps 6;
 QY 14 CIPQLRCSNTP-PLTCQRYCCYFDSLHACPC--LRCSNTPCQYCCPHSYFDSLH 70
 Db 48 CTPKVCPCPTPCPCATCPAAC-----ACPCPMKPCCTKCT-CC-----PRKCT 91
 QY 71 ACPEATC--OPYC 81
 Db 92 CCQPTCCVQPTC 104

Search completed: November 12, 2003, 06:26:59
 Job time : 38 secs